SEQUENCE LISTING

<110> Hartley, James L.

       Brasch, Michael A.

       Temple, Gary F.

       Cheo, David

<120> Compositions and Methods for Use in
       Recombinational Cloning of Nucleic Acids

<130> 0942.4680003

<140> 09/517,466

<141> 2000-03-02

<150> US 60/122,389

<151> 1999-03-02

<150> US 60/126,049

<151> 1999-03-23

<150> US 60/136,744

<151> 1999-05-28

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<170> PatentIn version 3.1

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ttttacgttt ctcgttcagc ttttttgtac aaagttggca ttataaaaaa gcattgctca   180

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<222> (655)..(754)

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atcgtctgtt tgtggatgta cagagtgata ttattgacac gcccgggcga cggatagtga   420

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<211> 22

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<210> 165

<211> 23

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<213> attR1 Reading Frame C

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<210> 166

<211> 21

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<211> 23

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acggtatacg gccttccttc cagttacttg aatttgaaat aaaaaaagtt tgccgctttg    4140

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gttcatgata acttcatgaa taatgaaatc acggctagta aaattgatga tggtaataat    4500

tcaaaaccac tgtcacctgg ttggacggac caaactgcgt ataacgcgtt tggaatcact    4560

acagggatgt ttaataccac tacaatggat gatgtatata actatctatt cgatgatgaa    4620

gatacccac caaacccaaa aaaagagggt gggtcgatca caagtttgta caaaaaagca    4680

ggcttgtcga ccccgggaat tcagatctac tagtgcggcc gcacgcgtac ccagctttct    4740

tgtacaaagt ggtgacgtcg agctctaagt aagtaacggc cgccaccgcg gtggagcttt    4800

ggacttcttc gccagaggtt tggtcaagtc tccaatcaag gttgtcggct tgtctacctt    4860
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gccagaaatt tacgaaaaga tggaaaaggg tcaaatcgtt ggtagatacg ttgttgacac   4920

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gcggtatttc acaccgcagg caagtgcaca aacaatactt aaataaatac tactcagtaa   6000

taacctattt cttagcattt ttgacgaaat ttgctatttt gttagagtct tttacaccat   6060

ttgtctccac acctccgctt acatcaacac caataacgcc atttaatcta agcgcatcac   6120

caacattttc tggcgtcagt ccaccagcta acataaaatg taagctttcg gggctctctt   6180

gccttccaac ccagtcagaa atcgagttcc aatccaaaag ttcacctgtc ccacctgctt   6240

ctgaatcaaa caagggaata aacgaatgag gtttctgtga agctgcactg agtagtatgt   6300

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cttgccacga ctcatctcca tgcagttgga cgatatcaat gccgtaatca ttgaccagag   6420

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aactattttt atatgctttt acaagacttg aaattttcct tgcaataacc gggtcaattg   6540

ttctctttct attgggcaca catataatac ccagcaagtc agcatcggaa tctagagcac   6600

attctgcggc ctctgtgctc tgcaagccgc aaactttcac caatggacca gaactacctg   6660

tgaaattaat aacagacata ctccaagctg cctttgtgtg cttaatcacg tatactcacg   6720
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tgctcaatag tcaccaatgc cctccctctt ggccctctcc ttttcttttt tcgaccgaat   6780

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acatatatta cgatgctgtc tattaaatgc ttcctatatt atatatatag taatgtcgtt   6960

tatggtgcac tctcagtaca atctgctctg atgccgcata gttaagccag ccccgacacc   7020

cgccaacacc cgctgacgcg ccctgacggg cttgtctgct cccggcatcc gcttacagac   7080

aagctgtgac cgtctccggg agctgcatgt gtcagaggtt ttcaccgtca tcaccgaaac   7140

gcgcga                                                             7146
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<210> 185

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR1A multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>


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<400> 185
act ttg tac aaa aaa gca ggc ttt aaa gga acc aat tca gtc gac tgg    48
Thr Leu Tyr Lys Lys Ala Gly Phe Lys Gly Thr Asn Ser Val Asp Trp
1               5                   10                  15

                                                                   64
atc cgg tac cga att c
Ile Arg Tyr Arg Ile
            20
```

<210> 186

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR1A multiple cloning site

<400> 186

```
Thr Leu Tyr Lys Lys Ala Gly Phe Lys Gly Thr Asn Ser Val Asp Trp
1               5                  10                 15

Ile Arg Tyr Arg Ile
            20
```

<210> 187

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR1A multiple cloning site

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<400>  187
gaattcgcgg ccgcactcga gatatctaga cccagctttc ttgtacaaa          49
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<210> 188

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<220>

<221> CDS

<222> (1)..(60)

<223>


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<400>  188
ttg tac aaa aaa gca ggc tgg cgc cgg aac caa ttc agt cga ctg gat     48
Leu Tyr Lys Lys Ala Gly Trp Arg Arg Asn Gln Phe Ser Arg Leu Asp
1               5                  10                 15
                                                                   62
ccg gta ccg aat tc
Pro Val Pro Asn
            20
```

<210> 189

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<400> 189

Leu Tyr Lys Lys Ala Gly Trp Arg Arg Asn Gln Phe Ser Arg Leu Asp
1   5   10   15

Pro Val Pro Asn
            20

<210> 190

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 190
g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa   49
  Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
  1   5   10   15
                                                                     50
g

<210> 191

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<400> 191

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1   5   10   15

<210> 192

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 192
ttg tac aaa aaa gca ggc tct tta aag gaa cca att cag tcg act gga   48
Leu Tyr Lys Lys Ala Gly Ser Leu Lys Glu Pro Ile Gln Ser Thr Gly
1   5   10   15

tcc ggt acc gaa ttc gatcgc   69
Ser Gly Thr Glu Phe
            20

<210> 193

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<400> 193

Leu Tyr Lys Lys Ala Gly Ser Leu Lys Glu Pro Ile Gln Ser Thr Gly
1   5   10   15

Ser Gly Thr Glu Phe
                20

<210> 194

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 194
g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa   49
  Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
  1   5   10   15
                                                                        50
g

<210> 195

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<400> 195

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1   5   10   15

<210> 196

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 196
ttg tac aaa aaa gca ggc tcc acc atg gga acc aat tca gtc gac tgg   48
Leu Tyr Lys Lys Ala Gly Ser Thr Met Gly Thr Asn Ser Val Asp Trp
1   5   10   15

atc cgg tac cga att c   64
Ile Arg Tyr Arg Ile
            20

<210> 197

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<400> 197

Leu Tyr Lys Lys Ala Gly Ser Thr Met Gly Thr Asn Ser Val Asp Trp
1   5   10   15

Ile Arg Tyr Arg Ile
            20

<210> 198

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 198
g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa   49
  Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
  1   5   10   15

                                                                    50
g

<210> 199

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<400> 199

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1   5   10   15

<210> 200

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 200

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ttg tac aaa aaa gca ggc ttt cat atg gga acc aat tca gtc gac tgg      48
Leu Tyr Lys Lys Ala Gly Phe His Met Gly Thr Asn Ser Val Asp Trp
1               5               10                  15

atc cgg tac cga att cgc                                              66
Ile Arg Tyr Arg Ile
            20
```


<210> 201

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<400> 201

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Leu Tyr Lys Lys Ala Gly Phe His Met Gly Thr Asn Ser Val Asp Trp
1               5               10                  15


Ile Arg Tyr Arg Ile
            20
```


<210> 202

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<400> 202

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agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g           51
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<210> 203

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<220>

<221> CDS

<222> (1)..(60)

<223>

<400> 203
```
ttg tac aaa aaa gca ggc tgc atg cga acc aat tca gtc gac tgg atc      48
Leu Tyr Lys Lys Ala Gly Cys Met Arg Thr Asn Ser Val Asp Trp Ile
1               5               10              15
                                                                     63
cgg tac cga att cgc
Arg Tyr Arg Ile
            20
```

<210> 204

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<400> 204

```
Leu Tyr Lys Lys Ala Gly Cys Met Arg Thr Asn Ser Val Asp Trp Ile
1               5               10              15


Arg Tyr Arg Ile
            20
```

<210> 205

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<400> 205
agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g   51

<210> 206

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<220>

<221> CDS

<222> (1)..(81)

<223>

<400> 206
ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga acc gtt   48
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Val
1   5   10   15

tca tgc atc gtc gac tgg atc cgg tac cga att cgc   84
Ser Cys Ile Val Asp Trp Ile Arg Tyr Arg Ile
                20   25

<210> 207

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<400> 207

Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Val
1   5   10   15

Ser Cys Ile Val Asp Trp Ile Arg Tyr Arg Ile
            20   25

<210> 208

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<400> 208
agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g   51

<210> 209

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR8 multiple cloning site

<220>

<221> CDS

<222> (1)..(78)

<223>

<400> 209
ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga acc atg   48
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Met
1   5   10   15

                                                                         81
gac cta gtc gac tgg atc cgg tac cga att cgc
Asp Leu Val Asp Trp Ile Arg Tyr Arg Ile
            20   25

<210> 210

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR8 multiple cloning site

<400> 210

Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Met
1   5   10   15

Asp Leu Val Asp Trp Ile Arg Tyr Arg Ile
            20   25

<210> 211

<211> 51

<212> DNA

<213> Artifical Sequence

<400> 211
agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g   51

<210> 212

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<220>

<221> CDS

<222> (1)..(78)

<223>

<400> 212

```
ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga cat atg          48
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly His Met
1               5                   10                  15

aga tct gtc gac tgg atc cgg tac cga att cgc                              81
Arg Ser Val Asp Trp Ile Arg Tyr Arg Ile
            20              25
```

<210> 213

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<400> 213

```
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly His Met
1               5                   10                  15

Arg Ser Val Asp Trp Ile Arg Tyr Arg Ile
            20              25
```

<210> 214

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<400> 214
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agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g          51
```

<210> 215

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<220>

<221> CDS

<222> (1)..(81)

<223>

<400> 215
ttg tac aaa aaa gca ggc ttc gaa cta agg aaa tac tta cat atg gga   48
Leu Tyr Lys Lys Ala Gly Phe Glu Leu Arg Lys Tyr Leu His Met Gly
1   5   10   15

acc aat tca gtc gac tgg atc cgg tac cga att cgc   84
Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile
            20   25

<210> 216

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 216

Leu Tyr Lys Lys Ala Gly Phe Glu Leu Arg Lys Tyr Leu His Met Gly
1   5   10   15

Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile
            20   25

<210> 217

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 217
agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g   51

<210> 218

<211> 88

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<220>

<221> CDS

<222> (1)..(87)

<223>

<400> 218
ttg tac aaa aaa gca ggc ttc gaa gga gat aga acc aat tct cta agg   48
Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1   5   10   15

aaa tac tta acc atg gtc gac tgg atc cgg tac cga att c   88
Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
            20   25

<210> 219

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 219

Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1   5   10   15

Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
            20   25

<210> 220

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 220
g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa   49
  Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
  1   5   10   15

g   50

<210> 221

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 221

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1   5   10   15

<210> 222

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST1

<400> 222
atgagctgtt gacaattaat catccggctc gtataatgtg tggaattgtg agcggataac   60

aatttcacac aggaaacaga caggtatagg atcacaagtt tgtacaaaaa agctgaacga   120

<210> 223

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST2

<220>

<221> CDS

<222> (94)..(135)

<223>

<400> 223
aatattctga aatgagctgt tgacaattaa tcatccggtc cgtataatct gtggaattgt   60

gagcggataa caatttcaca caggaaacag acc atg tcg tac tac cat cac cat   114
                                        Met Ser Tyr Tyr His His His
                                        1   5

cac cat cac ggc atc aca agt ttgtacaaaa aagctgaa   153
His His His Gly Ile Thr Ser
          10

<210> 224

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST2

<400> 224

```
Met Ser Tyr Tyr His His His His His His Gly Ile Thr Ser
1               5                   10
```

<210> 225

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST3

<220>

<221> CDS

<222> (106)..(120)

<223>


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<400> 225
cggttctggc aaatattctg aaatgagctg ttgacaatta atcatcggct cgtataatgt      60

gtggaattgt gagcggataa caatttcaca caggaaacag tattc atg tcc cct ata     117
                                                  Met Ser Pro Ile
                                                   1

                                                                        153
cta ggttattgga aaattaaggg ccttgtgcaa ccc
Leu
5
```

<210> 226

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST3

<400> 226

```
Met Ser Pro Ile Leu
1               5
```

<210> 227

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST3

<220>

<221> CDS

<222> (10)..(63)

<223>

<400> 227
ctggttccg cgt gga tct cgt cgt gca tct gtt gga tcc cca tca aca agt   51
        · Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser
          1   5   10

ttg tac aaa aaa gctgaacgag aaacgtaaaa tgatataaat atcaatata   102
Leu Tyr Lys Lys
15

<210> 228

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST3

<400> 228

Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser Leu Tyr
1   5   10   15

Lys Lys

<210> 229

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST4

<220>

<221> CDS

<222> (97)..(246)

<223>

<400> 229
gcaaatattc tgaaatgagc tgttgacaat taatcatccg gtccgtataa tctgtggaat 60

tgtgagcgga taacaatttc acacaggaaa cagacc atg ggt cat cat cat cat 114
                                         Met Gly His His His His
                                         1   5

cat cac gat tac gat atc cca acg acc gaa aac ctg tat ttt cag ggc 162
His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn Leu Tyr Phe Gln Gly
            10   15   20

gcc cat atg agc gat aaa att att cac ctg act gac gac agt gat gac 210
Ala His Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Asp Asp
        25   30   35

gat gac aag gta ccc atc aca agt ttg tac aaa aaa gctgaacga 255
Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr Lys Lys
    40   45   50

<210> 230

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST4

<400> 230

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu
1   5   10   15

Asn Leu Tyr Phe Gln Gly Ala His Met Ser Asp Lys Ile Ile His Leu
            20   25   30

Thr Asp Asp Ser Asp Asp Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr
      35   40   45

Lys Lys
   50

<210> 231

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST5

<400> 231
aggcaccccca ggctttacac tttatgcttc cggctcgtat gttgtgtgga attgtgagcg   60

gataacaatt tcacacagga aacagctatg accatgatta cgccaagctc taatacgact   120

cactataggg aaagctggta cgcctgcagg taccggtccg gaattcccgg gtcgacgatc   180
                                                                  204
acaagtttgt acaaaaaagc tgaa

<210> 232

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST5

<400> 232
tttacgtttc tcgttcagct ttcttgtaca aagtggtgat cactagtcgg cggccgctct   60

agaggatcca agcttacgta cgcgtgcatg cgacgtcata gctcttctat agtgtcacct   120

aaattcaatt cactggccgt cgttttacaa cgtcgtgact gggaaaaccc tggcgttacc   180
                                                                 204
caacttaatc gccttgcagc acat

<210> 233

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST6

<400> 233
taacgccagg gttttcccag tcacgacgtt gtaaaacgac ggccagtgaa ttgaatttag   60

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagcttg gatcctctag   120

agcggccgcc gactagtgat cacaagtttg tacaaaaaag ctgaacgaga aacgtaaaat   180

gatataaata tcaatatatt aaat   204

<210> 234

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST6

<400> 234
tatttatatc attttacgtt tctcgttcag ctttcttgta caaagtggtg atcgtcgacc   60

cgggaattcc ggaccggtac ctgcaggcgt accagctttc cctatagtga gtcgtattag   120

agcttggcgt aatcatggtc atagctgttt cctgtgtgaa attgttatcc gctcacaatt   180

ccacacaaca tacgagccgg aagcataaag tgtaaagcct ggggtgccta atgagtgagc   240

taactcacat taatt   255

<210> 235

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST7

<400> 235
ccattgacgc aaatgggcgg taggcgtgta cggtgggagg tctatataag cagagctcgt   60

ttagtgaacc gtcagatcgc ctggagacgc catccacgct gttttgacct ccatagaaga   120

```
caccgggacc gatccagcct ccggactcta gcctaggccg cggagcggat aacaatttca    180

cacaggaaac agctatgacc actaggcttt tgcaaaaagc tatttaggtg acactataga    240

aggtacgcct gcaggtaccg gtccggaatt cccatcacaa gtttgtacaa aaaagctgaa    300

                                                                    306
cgagaa
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<210> 236

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST8

<400> 236
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cgtatactcc ggaatattaa tagatcatgg agataattaa aatgataacc atctcgcaaa     60

taaataagta ttttactgtt ttcgtaacag ttttgtaata aaaaaaccta taaatattcc    120

ggattattca taccgtccca ccatcgggcg cggatcatca caagtttgta caaaaaagct    180
                                                                    204
gaacgagaaa cgtaaaatga tata
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<210> 237

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST9

<400> 237
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ttggcgaggg acattaaggc gtttaagaaa ttgagaggac ctgttataca cctctacggc     60

ggtcctagat tggtgcgtta atacacagaa ttctgattgg atcccggtcc gaagcgcgct    120
                                                                    153
ttcccatcaa caagtttgta caaaaaagct gaa
```

<210> 238

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST10

<220>

<221> CDS

<222> (109)..(201)

<223>

<400> 238
aaataagtat tttactgttt tcgtaacagt tttgtaataa aaaaacctat aaatattccg   60

gattattcat accgtcccac catcgggcgc ggatctcggt ccgaaacc atg tcg tac   117
                                                        Met Ser Tyr
                                                        1

tac cat cac cat cac cat cac gat tac gat atc cca acg acc gaa aac   165
Tyr His His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn
    5   10   15

ctg tat ttt cag ggc atc aca agt ttg tac aaa aaa gct   204
Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys Ala
20   25   30

<210> 239

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST10

<400> 239

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1   5   10   15

Thr Glu Asn Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys
            20   25   30

<210> 240

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST11

<400> 240
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tagtgaaccg tcagatcgcc tggagacgcc atccacgctg ttttgacctc catagaagac    60

accgggaccg atccagcctc cgcggccccg aattcgagct cggtacccgg ggatcctcta   120

gagtcgaggt cgacggtatc gataagcttg atatcaacaa gtttgtacaa aaaagctgaa   180
                                                                    204
cgagaaacgt aaaatgatat aaat
```

<210> 241

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST12.2

<400> 241
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accgtcagat cgcctggaga cgccatccac gctgttttga cctccataga agacaccggg    60

accgatccag cctccggact ctagcctagg ccgcggagcg dataacaatt tcacacagga   120

aacagctatg accattaggc ctttgcaaaa agctatttag gtgacactat agaaggtacg   180

cctgcaggta ccggtccgga attcccatca acaagtttgt acaaaaaagc tgaacgagaa   240
                                                                    255
acgtaaaatg atata
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<210> 242

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST13

<400> 242
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tgggcaaacc aagacagcta aagatctctc acctaccaaa caatgccccc ctgcaaaaaa    60

taaattcata taaaaaacat acagataacc atctgcggtg ataaattatc tctggcggtg   120
```

ttgacataaa taccactggc ggtgatactg agcacatcag caggacgcac tgaccaccat   180

gaaggtgacg ctcttaaaaa ttaagccctg aagaagggca gcattcaaag cagaaggctt   240

tggggtgtgt gatacgaaac gaagcattgg gatcatcaca agtttgtaca aaaaagctga   300

<210> 243

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST14

<400> 243
tgccggccac gatgcgtccg gcgtagagga tcgagatctc gatcccgcga aattaatacg   60

actcactata gggagaccac aacggtttcc ctctagatca caagtttgta caaaaaagct   120

<210> 244

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> misc_feature

<222> (1)..(1)

<223> may be any nucleotide

<220>

<221> CDS

<222> (106)..(120)

<223>

<400> 244

natcgagatc tcgatċccgc gaaattaata cgactcacta tagggagacc acaacggttt   60

ccctctagaa ataattttgt ttaactttaa gaaggagata tacat atg tcc cct ata   117
                                                              Met Ser Pro Ile
                                                              1

cta ggttattgga aaattaaggg ccttgtgcaa cccactcgac ttctttttgga   170
Leu
5

atatcttgaa gaaaaatatg aagagcattt gtat   204

<210> 245

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> misc_feature

<222> (1)..(1)

<223> may be any nucleotide

<400> 245

Met Ser Pro Ile Leu
1   5

<210> 246

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> CDS

<222> (70)..(99)

<223>

<400> 246
cagggctggc aagccacgtt tggtggtggc gaccatcctc caaaatcgga tctggttccg   60

cgtccatgg tcg aat caa aca agt ttg tac aaa aaa gct gaacgagaaa   109
          Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
          1   5   10

cgtaaaatga tataaatatc aatatattaa attagatttt gcat   153

<210> 247

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<400> 247

Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1   5   10

<210> 248

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<220>

<221> CDS

<222> (100)..(111)

<223>

<400> 248
gatctcgatc ccgcgaaatt aatacgactc actataggga gaccacaacg gtttccctct   60

agaaataatt ttgtttaact ttaagaagga gatatacat atg agc gat aaa   111
                                             Met Ser Asp Lys
                                             1

attattcacc tgactgacga cagttttgac acggatgtac tc   153

<210> 249

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 249

Met Ser Asp Lys
1

<210> 250

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<220>

<221> CDS

<222> (82)..(123)

<223>

<400> 250
gtggcggcaa ccaaagtggg tgcactgtct aaaggtcagt tgaaagagtt cctcgacgct   60

aacctggccg gttctggttc t ggt gat gac gat gac aag atc aca agt ttg   111
                         Gly Asp Asp Asp Asp Lys Ile Thr Ser Leu
                         1   5   10

tac aaa aaa gct gaacgagaaa cgtaaaatga tataaatatc   153
Tyr Lys Lys Ala

<210> 251

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 251

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Gly Asp Asp Asp Asp Lys Ile Thr Ser Leu Tyr Lys Lys Ala
1               5                  10
```


<210> 252

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<220>

<221> CDS

<222> (94)..(153)

<223>


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<400> 252
gatcccgcga aattaatacg actcactata gggagaccac aacggtttcc ctctagaaat    60

aattttgttt aactttaaga aggagatata cat atg tcg tac tac cat cac cat   114
                                       Met Ser Tyr Tyr His His His
                                       1                   5

cac cat cac ctc gaa tca aca agt ttg tac aaa aaa gct              153
His His His Leu Glu Ser Thr Ser Leu Tyr Lys Lys Ala
        10              15              20
```


<210> 253

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<400> 253

Met Ser Tyr Tyr His His His His His His Leu Glu Ser Thr Ser Leu
1   5   10   15

Tyr Lys Lys Ala
            20

<210> 254

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST18 p10 Promoter

<400> 254
gaagacctcg gccgtcgcgg cgcttgccgg tggtgctgac cccggatgaa gtggttcgca   60

tcctcggttt tctggaaggc gagcatcgtt tgttcgccca ggactctagc tatagttcta   120

gtggttggct acgtatcgag caagaaaata aaacgccaaa cgcgttggag tcttgtgtgc   180

tatttttaca aagattcaga aatacgcatc acttacaaca aggggggacta tgaaattatg   240

cattttgagg atgccgggac ctttaattca acccaacaca atatattata gttaaataag   300

aattatttat caaatcattt gtatattaat taaaatacta tactgtaaat tacatttttat   360

ttacaatgag gatcatcaca agtttgtaca aaaaagctga acgagaaacg taaaatgata   420

<210> 255

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST19 39K Promoter

<400> 255
ggtgacgccg tcatctttcc attgtaacgt aaatggcaac ttgtagatga acgcgctgtc   60

aaaaaaccgg ccagtttctt ccacaaactc gcgcacggct gtctcgtaaa cttttgcgtc   120

```
gcaacaatcg cgatgacctc gtggtatgga aatttttct aaaaaagtgt cgttcatgtc      180

ggcggcggcg ttcgcgctcc ggtacgcgcg acgggcacac agcaggacag ccttgtccgg      240

ctcgattatc ataaacaatc ctgcaggcat gcaagctgga tcatcacaag tttgtacaaa      300
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<210> 256

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<220>

<221> CDS

<222> (163)..(174)

<223>

<400> 256
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ggctacgtat actccggaat attaatagat catggagata attaaaatga taaccatctc      60

gcaaataaat aagtatttta ctgttttcgt aacagttttg taataaaaaa acctataaat     120

attccggatt attcataccg tcccaccatc gggcgcggat cc atg gcc cct ata        174
                                               Met Ala Pro Ile
                                               1

ctaggttatt ggaaaattaa gggccttgtg                                      204
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<210> 257

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<400> 257

Met Ala Pro Ile
1

<210> 258

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<220>

<221> CDS

<222> (1)..(48)

<223>

<400> 258
tcg gat ctg gtt ccg cgt cat aat caa aca agt ttg tac aaa aaa gct   48
Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1   5   10   15

gaacgagaaa cgtaaaatga tataaatatc aatatattaa attagat   95

<210> 259

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<400> 259

Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1   5   10   15

<210> 260

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<220>

<221> CDS

<222> (163)..(180)

<223>

<400> 260
ttgccgcttt gctatcaagt ataaatagac ctgcaattat taatctttttg tttcctcgtc   60

attgttctcg ttccctttct tccttgtttc tttttctgca caatatttca agctatacca   120

agcatacaat caactccaag cttgaagcaa gcctcctgaa ag atg aag cta ctg   174
                                              Met Lys Leu Leu
                                               1

tct tct atcgaacaag catgcgatat ttgc   204
Ser Ser
5

<210> 261

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<400> 261

Met Lys Leu Leu Ser Ser
1   5

<210> 262

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<220>

<221> CDS

<222> (37)..(78)

<223>

<400> 262
gaagagagta gtaacaaagg tcaaagacag ttgact gta tcg tcg agg tcg aat   54
                                          Val Ser Ser Arg Ser Asn
                                          1   5

caa aca agt ttg tac aaa aaa gct gaacgagaaa cgtaaaatga tata   102
Gln Thr Ser Leu Tyr Lys Lys Ala
            10

<210> 263

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<400> 263

Val Ser Ser Arg Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1   5   10

<210> 264

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST22 Promoter region

<220>

<221> CDS

<222> (217)..(228)

<223>

<400> 264
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acgcacacta ctctctaatg agcaacggta tacggccttc cttccagtta cttgaatttg    60

aaataaaaaa agtttgccgc tttgctatca agtataaata gacctgcaat tattaatctt   120

ttgtttcctc gtcattgttc tcgttccctt tcttccttgt ttctttttct gcacaatatt   180

                                                                    228
tcaagctata ccaagcatac aatcaactcc aagctt atg ccc aag aag
                                            Met Pro Lys Lys
                                            1

                                                                    255
aagcggaagg tctcgagcgg cgccaat
```

<210> 265

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST22 Promoter region

<400> 265

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Met Pro Lys Lys
1
```

<210> 266

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST22

<220>

<221> CDS

<222> (28)..(66)

<223>

<400> 266
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                                                                    54
gaagataccc caccaaaccc aaaaaaa gag ggt ggg tcg aat caa aca agt ttg
                             Glu Gly Gly Ser Asn Gln Thr Ser Leu
```

```
                               1               5
                                                                    82
tac aaa aaa gct gaacgagaaa cgtaaa
Tyr Lys Lys Ala
10
```

<210> 267

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST22

<400> 267

```
Glu Gly Gly Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1               5                   10
```

<210> 268

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 268
```
atcccgcgaa attaatacga ctcactatag ggagaccaca acggtttccc tctagatcac    60

aagtttgtac aaaaaagctg aacgagaaac gtaaaatgat at                      102
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<210> 269

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<220>

<221> CDS

<222> (61)..(126)

<223>

<400> 269
tttttatgca aaatctaatt taatatattg atatttatat cattttacgt ttctcgttca   60

gct ttc ttg tac aaa gtg gtg att atg tcg tac tac cat cac cat cac   108
Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
1   5   10   15

cat cac ctc gat gag caa taactagcat aacccccttgg ggcctct   153
His His Leu Asp Glu Gln
            20

<210> 270

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 270

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
1   5   10   15

His His Leu Asp Glu Gln
            20

<210> 271

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST24 T7 promoter

<400> 271
atcgagatct cgatcccgcg aaattaatac gactcactat agggagacca caacggtttc   60

cctctagatc acaagtttgt acaaaaaagc tgaacgagaa ac   102

<210> 272

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST24 T7 promoter

<220>

<221> CDS

<222> (22)..(60)

<223>

<400> 272
tcattttacg tttctcgttc a gct ttc ttg tac aaa gtg gtg att atg tcc   51
                         Ala Phe Leu Tyr Lys Val Val Ile Met Ser
                         1   5   10

cct ata cta ggttattgga aaattaaggg ccttgtgcaa cccactcgac tt   102
Pro Ile Leu

<210> 273

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST24 T7 promoter

<400> 273

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Pro Ile Leu
1   5   10

<210> 274

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<220>

<221> misc_feature

<222> (1)..(1)

<223> May be any nucleotide

<400> 274
nagatctcga tcccgcgaaa ttaatacgac tcactatagg gagaccacaa cggtttccct   60

ctagatcaca agtttgtaca aaaaagctga acgagaaacg ta   102

<210> 275

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<220>

<221> CDS

<222> (19)..(60)

<223>

<400> 275
ttttacgttt ctcgttca gct ttc ttg tac aaa gtg gtg att atg agc gat   51
                     Ala Phe Leu Tyr Lys Val Val Ile Met Ser Asp
                     1   5   10

aaa att att cacctgactg acgacagttt tgacacggat gtactcaaag cg   102
Lys Ile Ile

<210> 276

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<400> 276

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Asp Lys Ile Ile
1   5   10

<210> 277

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST26 CMV promoter

<220>

<221> CDS

<222> (238)..(297)

<223>

<400> 277
ttgacgtcaa tgggagtttg ttttggcacc aaaatcaacg ggactttcca aaatgtcgta   60

acaactccgc cccattgacg caaatgggcg gtaggcgtgt acggtgggag gtctatataa   120

gcagagctcg tttagtgaac cgtcagatcg cctggagacg ccatccacgc tgttttgacc   180

tccatagaag acaccgggac cgatccagcc tccggactct agcctaggcc gcggacc   237

atg gcg tac tac cat cac cat cac cat cac tct aga tca aca agt ttg   285
Met Ala Tyr Tyr His His His His His His Ser Arg Ser Thr Ser Leu
1   5   10   15

                                                                      306
tac aaa aaa gct gaacgagaa
Tyr Lys Lys Ala
            20

<210> 278

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST26 CMV promoter

<400> 278

Met Ala Tyr Tyr His His His His His His Ser Arg Ser Thr Ser Leu
1   5   10   15

Tyr Lys Lys Ala
            20

<210> 279

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST27 promoter

<220>

<221> misc_feature

<222> (1)..(1)

<223> May be any nucleotide

<220>

<221> CDS

<222> (139)..(153)

<223>

<400> 279
nacggtggga ggtctatata agcagagctc gtttagtgaa ccgtcagatc gcctggagac   60

gccatccacg ctgttttgac ctccatagaa gacaccggga ccgatccagc ctccggactc   120

tagcctaggc cgcggacc atg gcc cct ata cta ggttattgga aaattaaggg   173
                    Met Ala Pro Ile Leu
                    1   5

ccttgtgcaa cccactcgac ttcttttgga atatcttgaa gaaaaatatg aagagcattt   233

gtatgagcgc gatgaaggtg at   255

<210>   280

<211>   5

<212>   PRT

<213>   Artificial Sequence

<220>

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<223>   May be any nucleotide

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Met Ala Pro Ile Leu
1   5

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Thr Ser Leu Tyr Lys Lys Ala

10

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tcactagtcg gcggccgctc tagagtatcc ctcgaggggc ccaagcttac gcgtaccag   300

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                                  1                   5

cat cac ggc atc aca agt ttg tac aaa aaa gca ggc ttt gaa aac ctg        102
His His Gly Ile Thr Ser Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu
        10              15                  20

tat ttt caa gga acc atg gag aaa aaa atc act gga tat acc acc gtt        150
Tyr Phe Gln Gly Thr Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val
25              30                  35                  40

gat                                                                     153
Asp
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Lys Ile Thr Gly Tyr Thr Thr Val Asp
                35                  40
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